

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

10 (i) APPLICANT: Jessell, Thomas M.
Basler, Konrad
Yomada, Toshiya

15 (ii) TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF
DORSALIN-1

(iii) NUMBER OF SEQUENCES: 18

20 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham
(B) STREET: 30 Rockefeller Plaza
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States of America
(F) ZIP: 10112

25 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

35 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 0576/40314

40 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 977-9550
(B) TELEFAX: (212) 664-0525
(C) TELEX: 422523 COOP UI

45 (2) INFORMATION FOR SEQ ID NO:1:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

60 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 91..1371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 CCTTTCCCTCT GTCTGTAAAG ATTCAACATT TTTAACAGT TAAAATACCT TGTCCTCTTG 60
TCTCTCCATC AGAAAGTAAA TACATAAGAA ATG CAT TAT TTT GGA GTA TTA GCT 114
Met His Tyr Phe Gly Val Leu Ala
1 5

10 GCA CTG TCT GTT TTC AAT ATC ATT GCC TGC CTG ACA AGA GGC AAG CCT 162
Ala Leu Ser Val Phe Asn Ile Ile Ala Cys Leu Thr Arg Gly Lys Pro
10 15 20

15 TTG GAA AAC TGG AAA AAG CTA CCA GTT ATG GAA GAG TCT GAT GCA TTC 210
Leu Glu Asn Trp Lys Lys Leu Pro Val Met Glu Glu Ser Asp Ala Phe
25 30 35 40

20 TTT CAT GAT CCT GGG GAA GTG GAA CAT GAC ACC CAC TTT GAC TTT AAA 258
Phe His Asp Pro Gly Glu Val Glu His Asp Thr His Phe Asp Phe Lys
45 50 55

25 TCT TTC TTG GAG AAT ATG AAG ACA GAT TTA CTA AGA AGT CTG AAT TTA 306
Ser Phe Leu Glu Asn Met Lys Thr Asp Leu Leu Arg Ser Leu Asn Leu
60 65 70

30 TCA AGG GTC CCC TCA CAA GTG AAG ACC AAA GAA GAG CCA CCA CAG TTC 354
Ser Arg Val Pro Ser Gln Val Lys Thr Lys Glu Glu Pro Pro Gln Phe
75 80 85

35 ATG ATT GAT TTA TAC AAC AGA TAT ACA GCG GAC AAG TCC TCC ATC CCT 402
Met Ile Asp Leu Tyr Asn Arg Tyr Thr Ala Asp Lys Ser Ser Ile Pro
90 95 100

40 GCA TCC AAC ATC GTG AGG AGC TTC AGC ACT GAA GAT GTT GTT TCT TTA 450
Ala Ser Asn Ile Val Arg Ser Phe Ser Thr Glu Asp Val Val Ser Leu
105 110 115 120

45 ATT TCA CCA GAA GAA CAC TCA TTT CAG AAA CAC ATC TTG CTC TTC AAC 498
Ile Ser Pro Glu Glu His Ser Phe Gln Lys His Ile Leu Leu Phe Asn
125 130 135

50 ATC TCT ATT CCA CGA TAT GAG GAA GTC ACC AGA GCT GAA CTG AGA ATC 546
Ile Ser Ile Pro Arg Tyr Glu Glu Val Thr Arg Ala Glu Leu Arg Ile
140 145 150

55 TTT ATC TCC TGT CAC AAG GAA GTT GGG TCT CCC TCC AGA CTG GAA GGC 594
Phe Ile Ser Cys His Lys Glu Val Gly Ser Pro Ser Arg Leu Glu Gly
155 160 165

60 AAC ATG GTC ATT TAT GAT GTT CTA GAT GGA GAC CAT TGG GAA AAC AAA 642
Asn Met Val Ile Tyr Asp Val Leu Asp Gly Asp His Trp Glu Asn Lys
170 175 180

65 GAA ACT ACC AAA TCT TTA CTT GTC TCT CAC AGT ATT CAG GAC TGT GGC 690
Glu Ser Thr Lys Ser Leu Leu Val Ser His Ser Ile Gln Asp Cys Gly
185 190 195 200

70 TGG GAG ATG TTT GAG GTG TCC AGC GCT GTG AAA AGA TGG GTC AAG GCA 738
Trp Glu Met Phe Glu Val Ser Ser Ala Val Lys Arg Trp Val Lys Ala
205 210 215

75 GAC AAG ATG AAG ACT AAA AAC AAG CTA GAG GTT GTT ATA GAG AGT AAG 786

	Asp Lys Met Lys Thr Lys Asn Lys Leu Glu Val Val Ile Glu Ser Lys	
	220 225 230	
5	GAT CTG AGT GGT TTT CCT TGT GGG AAG CTG GAT ATT ACT GTT ACT CAT Asp Leu Ser Gly Phe Pro Cys Gly Lys Leu Asp Ile Thr Val Thr His 235 240 245	834
10	GAC ACT AAA AAT CTG CCC CTA TTA ATA GTG TTC TCC AAT GAT CGC AGC Asp Thr Lys Asn Leu Pro Leu Leu Ile Val Phe Ser Asn Asp Arg Ser 250 255 260	882
15	AAT GGG ACA AAA GAG ACC AAA GTG GAG CTC CGG GAG ATG ATT GTT CAT Asn Gly Thr Lys Glu Thr Lys Val Glu Leu Arg Glu Met Ile Val His 265 270 275 280	930
20	GAA CAA GAA AGT GTG CTA AAC AAA TTA GGA AAG AAC GAC TCT TCA TCT Glu Gln Glu Ser Val Leu Asn Lys Leu Gly Lys Asn Asp Ser Ser Ser 285 290 295	978
25	GAA GAA GAA CAG AGA GAA GAA AAA GCC ATT GCT AGG CCC CGT CAG CAT Glu Glu Glu Gln Arg Glu Glu Lys Ala Ile Ala Arg Pro Arg Gln His 300 305 310	1026
30	TCC TCC AGA AGC AAG AGA AGC ATA GGA GCA AAC CAC TGT CGG AGA ACG Ser Ser Arg Ser Lys Arg Ser Ile Gly Ala Asn His Cys Arg Arg Thr 315 320 325	1074
35	TCA CTC CAT GTG AAC TTT AAA GAA ATA CGT TGG GAT TCT TGG ATC ATT Ser Leu His Val Asn Phe Lys Glu Ile Gly Trp Asp Ser Trp Ile Ile 330 335 340	1122
40	GCA CCC AAA GAT TAT GAG GCT TTT GAG TGT AAA GGA GGT TGC TTC TTC Ala Pro Lys Asp Tyr Glu Ala Phe Glu Cys Lys Gly Gly Cys Phe Phe 345 350 355 360	1170
45	CCC CTC ACA GAT AAT GTT ACG CCA ACC AAA CAT GCT ATT GTC CAG ACT Pro Leu Thr Asp Asn Val Thr Pro Thr Lys His Ala Ile Val Gln Thr 365 370 375	1218
50	CTG GTG CAT CTC CAA AAC CCA AAG AAA GCT TCC AAG GCC TGT TGT GTT Leu Val His Leu Gln Asn Pro Lys Lys Ala Ser Lys Ala Cys Cys Val 380 385 390	1266
55	CCA ACT AAA TTG GAT GCA ATC TCT ATT CTT TAT AAG GAT GAT GCT GGT Pro Thr Lys Leu Asp Ala Ile Ser Ile Leu Tyr Lys Asp Asp Ala Gly 395 400 405	1314
60	GTG CCC ACT TTG ATA TAT AAC TAT GAA GGG ATG AAA GTG GCA GAA TGT Val Pro Thr Leu Ile Tyr Asn Tyr Glu Gly Met Lys Val Ala Glu Cys 410 415 420	1362
	GGC TGC AGG TAGTATATGC TGAATATCTA AGAATATACT CTTTCTGCT Gly Cys Arg 425	1411
	GTCTGTAAA CTGTACATTA GTGATGCAA TGAAAATCCT TGCAACAAAG GTTGGAGCA	1471
	CGGCATGGGG CTGGTTGTTG TTGCTGCTTT TAAAGGAAAG ATGGCATTAA AAGAACGGCA	1531
	ATCACTGTAA ATACCCCTGCA TTATATACCA TTAATTAAAA CTTTGTGAGA TTGAAAAAAA	1591
	AAAAAAAAAA AA	1603

10002278-11-000000

July 16
cont

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Tyr Phe Gly Val Leu Ala Ala Leu Ser Val Phe Asn Ile Ile
1 5 10 15

Ala Cys Leu Thr Arg Gly Lys Pro Leu Glu Asn Trp Lys Lys Leu Pro
20 25 30

Val Met Glu Glu Ser Asp Ala Phe Phe His Asp Pro Gly Glu Val Glu
20 35 40 45

His Asp Thr His Phe Asp Phe Lys Ser Phe Leu Glu Asn Met Lys Thr
50 55 60

Asp Leu Leu Arg Ser Leu Asn Leu Ser Arg Val Pro Ser Gln Val Lys
65 70 75 80

Thr Lys Glu Glu Pro Pro Gln Phe Met Ile Asp Leu Tyr Asn Arg Tyr
85 90 95

Thr Ala Asp Lys Ser Ser Ile Pro Ala Ser Asn Ile Val Arg Ser Phe
100 105 110

Ser Thr Glu Asp Val Val Ser Leu Ile Ser Pro Glu Glu His Ser Phe
115 120 125

Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg Tyr Glu Glu
130 135 140

Val Thr Arg Ala Glu Leu Arg Ile Phe Ile Ser Cys His Lys Glu Val
145 150 155 160

Gly Ser Pro Ser Arg Leu Glu Gly Asn Met Val Ile Tyr Asp Val Leu
165 170 175

Asp Gly Asp His Trp Glu Asn Lys Glu Ser Thr Lys Ser Leu Leu Val
180 185 190

Ser His Ser Ile Gln Asp Cys Gly Trp Glu Met Phe Glu Val Ser Ser
195 200 205

Ala Val Lys Arg Trp Val Lys Ala Asp Lys Met Lys Thr Lys Asn Lys
210 215 220

Leu Glu Val Val Ile Glu Ser Lys Asp Leu Ser Gly Phe Pro Cys Gly
225 230 235 240

Lys Leu Asp Ile Thr Val Thr His Asp Thr Lys Asn Leu Pro Leu Leu
245 250 255

Ile Val Phe Ser Asn Asp Arg Ser Asn Gly Thr Lys Glu Thr Lys Val
260 265 270

10002223445566778899

*Feb
16
CMT*

Glu Leu Arg Glu Met Ile Val His Glu Gln Glu Ser Val Leu Asn Lys
275 280 285

5 Leu Gly Lys Asn Asp Ser Ser Ser Glu Glu Gln Arg Glu Glu Lys
290 295 300

Ala Ile Ala Arg Pro Arg Gln His Ser Ser Arg Ser Lys Arg Ser Ile
305 310 315 320

10 Gly Ala Asn His Cys Arg Arg Thr Ser Leu His Val Asn Phe Lys Glu
325 330 335

Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Asp Tyr Glu Ala Phe
340 345 350

15 Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Thr Asp Asn Val Thr Pro
355 360 365

20 Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Gln Asn Pro Lys
370 375 380

Lys Ala Ser Lys Ala Cys Cys Val Pro Thr Lys Leu Asp Ala Ile Ser
385 390 395 400

25 Ile Leu Tyr Lys Asp Asp Ala Gly Val Pro Thr Leu Ile Tyr Asn Tyr
405 410 415

Glu Gly Met Lys Val Ala Glu Cys Gly Cys Arg
420 425

30 (2) INFORMATION FOR SEQ ID NO:3:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

55 Glu His Ser Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His
1 5 10 15

Asp Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys
20 25 30

55 His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu
35 40 45

Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro
50 55 60

60 Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu
65 70 75 80

Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val
									85			90			95
Asn	Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu
									100		105			110	
Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	Glu	Asn	Glu	Lys	Val	Val
									115		120		125		
Leu	Lys	Asn	Tyr	Gln	Asp	Met	Val	Val	Glu	Gly	Cys	Gly	Cys	Arg	
									130		135		140		

(2) INFORMATION FOR SEQ ID NO:4:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

 (iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(2) INFORMATION FOR SEQ ID NO:5:

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15 Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn
1 5 10 15

20 Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp
20 25 30

25 Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu Tyr
35 40 45

30 Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Lys
50 55 60

35 Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu Asn
65 70 75 80

40 Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
85 90 95

45 Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys
100 105 110

50 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile
115 120 125

55 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135 140

(2) INFORMATION FOR SEQ ID NO:6:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

60 Glu Cys Lys Asp Ile Gln Thr Phe Leu Tyr Thr Ser Leu Leu Thr Val
1 5 10 15

100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

Thr Leu Asn Pro Leu Arg Cys Lys Arg Pro Arg Arg Lys Arg Ser Tyr
20 25 30

5 Ser Lys Leu Pro Phe Thr Ala Ser Asn Ile Cys Lys Lys Arg His Leu
35 40 45

Tyr Val Glu Phe Lys Asp Val Gly Trp Gln Asn Trp Val Ile Ala Pro
50 55 60

10 Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly Glu Cys Pro Tyr Pro Leu
65 70 75 80

15 Thr Glu Ile Leu Asn Gly Ser Asn His Ala Ile Leu Gln Thr Leu Val
85 90 95

20 His Ser Ile Glu Pro Glu Asp Ile Pro Leu Pro Cys Cys Val Pro Thr
100 105 110

25 Lys Met Ser Pro Ile Ser Met Leu Phe Tyr Asp Asn Asn Asp Asn Val
115 120 125

30 Val Leu Arg His Tyr Glu Asn Met Ala Val Asp Glu Cys Gly Cys Arg
130 135 140

25 (2) INFORMATION FOR SEQ ID NO:7:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

40 (iii) HYPOTHETICAL: NO

45 (iv) ANTI-SENSE: NO

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

55 Gly Ala Asp Glu Glu Lys Glu Gln Ser His Arg Pro Phe Leu Met Leu
1 5 10 15

60 Gln Ala Arg Gln Ser Glu Asp His Pro His Arg Arg Arg Arg Gly
20 25 30

65 Leu Glu Cys Asp Gly Lys Val Asn Ile Cys Cys Lys Lys Gln Phe Phe
35 40 45

70 Val Ser Phe Lys Asp Ile Gly Trp Asn Asp Trp Ile Ile Ala Pro Ser
50 55 60

75 Gly Tyr His Ala Asn Tyr Cys Glu Gly Glu Cys Pro Ser His Ile Ala
65 70 75 80

80 Gly Thr Ser Gly Ser Ser Leu Ser Phe His Ser Thr Val Ile Asn His
85 90 95

85 Tyr Arg Met Arg Gly His Ser Pro Phe Ala Asn Leu Lys Ser Cys Cys

SUBMITTED BY THE NCBP

Sab
A6
Cont

	100	105	110
5	Val Pro Thr Lys Leu Arg Pro Met Ser Met Leu Tyr Tyr Asp Asp Gly		
	115	120	125
	Gln Asn Ile Ile Lys Lys Asp Ile Gln Asn Met Ile Val Glu Glu Cys		
	130	135	140
10	Gly Cys Ser		
	145		

(2) INFORMATION FOR SEQ ID NO:8:

- (1) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(IV) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30 Gly Met Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg
1 5 10 15

Ala Gln His Leu Gln Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn
20 25 30

55 Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr
35 40 45

Ile Asp Phe Arg Lys | Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys
50 55 60

40 Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys
50 55 60

Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser
65 70 75 80

45 Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn
85 90 95

Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro
100 105 110

Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu
115 120 125

Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
130 135

(2) INFORMATION FOR SEQ ID NO:9:

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 257 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
5 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
Asp Val Leu Glu Asp Ser Glu Thr Trp Asp Gln Ala Thr Gly Thr Lys
1 5 10 15
15 Thr Phe Leu Val Ser Gln Asp Ile Arg Asp Glu Gly Trp Glu Thr Leu
20 25 30
20 Glu Val Ser Ser Ala Val Lys Arg Trp Val Arg Ala Asp Ser Thr Thr
35 40 45
25 Asn Lys Asn Lys Leu Glu Val Thr Val Gln Ser His Arg Glu Ser Cys
50 55 60
30 Asp Thr Leu Asp Ile Ser Val Pro Pro Gly Ser Lys Asn Leu Pro Phe
65 70 75 80
35 Phe Val Val Phe Ser Asn Asp Arg Ser Asn Gly Thr Lys Glu Thr Arg
85 90 95
40 Leu Asp Leu Leu Lys Glu Met Ile Gly His Glu Gln Glu Thr Met Leu
100 105 110
45 Val Lys Thr Ala Lys Asn Ala Tyr Gln Gly Ala Gly Glu Ser Gln Glu
115 120 125
50 Glu Glu Gly Leu Asp Gly Tyr Thr Ala Val Gly Pro Leu Leu Ala Arg
130 135 140
55 Arg Lys Arg Ser Thr Gly Ala Ser Ser His Cys Gln Lys Thr Ser Leu
145 150 155 160
60 Arg Val Asn Phe Glu Asp Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro
165 170 175
65 Lys Glu Tyr Asp Ala Tyr Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu
180 185 190
70 Ala Asp Asp Val Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val
195 200 205
75 His Leu Lys Phe Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr
210 215 220
80 Lys Leu Ser Pro Ile Ser Ile Leu Tyr Lys Asp Asp Met Gly Val Pro
225 230 235 240
85 Thr Leu Lys Tyr His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys
245 250 255
90 Arg

*but
A 6 cont*

5 (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: YES

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGAATTCTG GVANGAYTGG ATHRTNGC

28

20 (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: YES

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGGATCCAR NGTYTGACD ATNGCRTG

28

35 (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: YES

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGGAATTCCAT CGATAACCGGA AGCTGAAGC

29

50 (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: YES

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

FBI - 2025 RELEASE UNDER E.O. 14176

*Surf
Ab
Cem*

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCGTCGACA TCGATATTCA GCATATACTA CC

10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGAATTCTGA TATCAGCTTC TGCTCTGCTC CTATGTTCT CTTGC

45

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA

40

(iii) HYPOTHETICAL: YES

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGAATTCTGA TATCCGAGGA GGACCTGAAC CACTGTCGGA GAACGTC

47

50

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Ile Gly Ala Glu Gln Lys Leu Ile Ser

SEARCHED
INDEXED
SERIALIZED
FILED

Sept 6 1987
AB
AMT

1

5

10

(2) INFORMATION FOR SEQ ID NO:17:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Ser Lys Arg
1

20

(2) INFORMATION FOR SEQ ID NO:18:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

35

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

SEARCHED
INDEXED
FILED